

SEQUENCE LISTING

<110> REGENTS OF THE UNIVERSITY OF CALIFORNIA
TSIEN, Roger
Campbell, Robert

<120> NON-OLIGOMERIZING FLUORESCENT PROTEINS

<130> REGEN1530-2

<140> Herewith

<141> 2001-05-24

<160> 29

<170> PatentIn version 3.0

<210> 1

<211> 716

<212> DNA

<213> Aequorea victoria

<220>

<221> CDS

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gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	

act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	

tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg aaa cag	240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
65 70 75 80	

cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	

act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	

aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	

gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	

104250-0540

130 135 140

tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat gga 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aaa gtt aac ttc aaa att aga cac aac att gaa gat gga agc gtt 528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct 576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcg 624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta 672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa ta 716
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 2
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<212> PRT
<213> Aequorea victoria

<400> 2

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

000653-052401

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

0906533-052401

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cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag				288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu				
	85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag				336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				
	100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc				384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				
	115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac				432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				
	130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac				480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn				
	145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc				528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser				
	165	170	175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc				576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly				
	180	185	190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg				624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu				
	195	200	205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc				672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe				
	210	215	220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa				720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys				
	225	230	235	

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<211> 239

<212> PRT

<213> Aequorea victoria

<400> 4

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

T04250" 0559360

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 5
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<220>
<221> CDS
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

1	5	10	15	
gtc gag ctg gac ggc gac gta aac ggc cac agg ttc agc gtg tcc ggc Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly	20	25	30	96
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	35	40	45	144
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	50	55	60	192
ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	65	70	75	240
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	85	90	95	288
cgt acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	100	105	110	336
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	125	384
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	130	135	140	432
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	145	150	155	480
ggc atc aag gcc cac ttc aag atc cgc cac aac atc gag gac ggc agc Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	165	170	175	528
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	180	185	190	576
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	195	200	205	624
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	210	215	220	672
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	225	230	235	720

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<212> PRT
 <213> Aequorea victoria

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

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Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
				5					10					15			
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96	
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
				20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144	
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
				35					40					45			
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192	
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
				50					55					60			
ttc	ggc	tac	ggc	gtg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240	
Phe	Gly	Tyr	Gly	Val	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65					70					75					80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288	
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
				85					90					95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
				100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384	
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
				115					120					125			
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432	
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
				130					135					140			
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480	
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145					150					155					160		
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528	
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
				165					170					175			
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
				180					185					190			

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 9
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

F01250-3599860

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

gag ggg agg cca tac gaa ggc cac aat acc gta aag ctt aag gta acc 200
Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val Thr
35 40 45

aag ggg gga cct ttg cca ttt gct tgg gat att ttg tca cca caa ttt 248
 Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
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 cag tat gga agc aag gta tat gtc aag cac cct gcc gac ata cca gac 296
 Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro Asp
 70 75 80
 tat aaa aag ctg tca ttt cct gaa gga ttt aaa tgg gaa agg gtc atg 344
 Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
 85 90 95
 aac ttt gaa gac ggt ggc gtc gtt act gta acc cag gat tcc agt ttg 392
 Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
 100 105 110
 cag gat ggc tgt ttc atc tac aag gtc aag ttc att ggc gtg aac ttt 440
 Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn Phe
 115 120 125
 cct tcc gat gga cct gtt atg caa aag aag aca atg ggc tgg gaa gcc 488
 Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
 130 135 140 145
 agc act gag cgt ttg tat cct cgt gat ggc gtg ttg aaa gga gag att 536
 Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu Ile
 150 155 160
 cat aag gct ctg aag ctg aaa gac ggt ggt cat tac cta gtt gaa ttc 584
 His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu Phe
 165 170 175
 aaa agt att tac atg gca aag aag cct gtg cag cta cca ggg tac tac 632
 Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr Tyr
 180 185 190
 tat gtt gac tcc aaa ctg gat ata aca agc cac aac gaa gac tat aca 680
 Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr
 195 200 205
 atc gtt gag cag tat gaa aga acc gag gga cgc cac cat ctg ttc ctt 728
 Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe Leu
 210 215 220 225
 taa ggctgaactt ggctcagacg tgggtgagcg gtaatgacca caaaaggcag 781
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 <213> Discosoma sp.

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0066530-05401

Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
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Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
35 40 45

Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
50 55 60

Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
65 70 75 80

Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
85 90 95

Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser
100 105 110

Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
130 135 140

Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
145 150 155 160

Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
165 170 175

Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
180 185 190

Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
195 200 205

Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
210 215 220

Leu
225

<210> 13
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<213> Artificial

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<212> DNA

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<212> DNA

<213> Artificial

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<210> 16

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<212> DNA

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36

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36

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 <223> PRIMER L221K/F223R top

<400> 19
 cacatcgctcc tgaaggagcg cgtgaccgcc gccggg

36

<210> 20
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> PRIMER L221K/F223R bottom

<400> 20
 cccggcgggcg gtcacgcgct ccttcaggac catgtg

36

<210> 21
 <211> 33
 <212> PRT
 <213> Artificial

<220>
 <223> ADDITIONAL 33 AMINO ACIDS TAG TO THE N-TERMINUS OF THE GFPs

<400> 21

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
 1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

Pro

<210> 22
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> PRIMER I125K

<400> 22
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33

090663 05401
 T04250 00000000

<210> 23
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> PRIMER I125K reverse

<400> 23
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33

<210> 24
 <211> 33
 <212> DNA
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<220>
 <223> PRIMER I125R forward

<400> 24
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33

<210> 25
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> PRIMER I125R reverse

<400> 25
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33

<210> 26
 <211> 18
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic peptide

<400> 26

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
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Lys Gly

<210> 27
 <211> 86
 <212> DNA
 <213> Artificial

<220>
 <223> Primer for PCR

T04250-05440

<400> 27
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 caaggaacag atggtggcgt ccctcg 86

<210> 28
 <211> 86
 <212> DNA
 <213> Artificial

<220>
 <223> Primer for PCR

<400> 28
 ccggatcccc cttggtgctg ccctccccgc tgccgggctt ccgctcccg ctggtgctgc 60
 ccaggaacag gtggtggcgg ccctcg 86

<210> 29
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> Primer for PCR

<400> 29
 gtacgacgat gacgataagg atcc 24

006530 05401
 104250 0359000